

GOING VIRAL: USING SOCIAL NETWORK THEORY TO EXPLORE THE SOCIAL DYNAMICS OF THE CASSAVA MOSAIC VIRUS PANDEMICS

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BACKGROUND and OBJECTIVES

Many crop diseases are propagated mechanically through infected stem cuttings that move along farmers' informal seed exchange networks. In Africa, the Cassava Mosaic Disease (CMD) and Cassava Brown Streak Disease (CBSD) are major threats to regional food security and cause vast economic losses to staple crops. CMD and CBSD both originated from East Africa but have been steadily expanding westwards towards Central and West Africa (Legg *et al.*, 2011). Successful control of crop pandemics requires a better understanding of the social factors that can enhance the spread of viruses through open and unrestricted seed exchanges or, on the contrary, slow down the adoption of pathogen-resistant cultivars through tighter social control of local seed systems.

MATERIAL and METHODS

Using a phylodynamic approach, we investigated how the spread of plant pathogens is influenced by local seed systems, by analysing spatial patterns of genetic variation in the African cassava mosaic virus (ACMV) in Gabon, central Africa. Viral diversity was characterized through DNA sequencing of the replication associated protein (Rep) open reading frame on the ACMV genome. Because genetic relationships between haplotypes not solely represent evolutionary ties but reflect also the movements of viral strains through regional networks of seed exchange, we analysed regional patterns of ACMV diversity not only from the point of view of population genetics but also from the point of view of social network analysis.

RESULTS

In small-scale farming communities, circulation of crop landraces is often channelled by social structures which determine the connectivity of farmer populations and, *in extenso*, favour or limit germplasm exchanges among communities (Delêtre *et al.*, 2011). We show that social structures leave distinctive molecular signals on intra- and inter-population levels of DNA polymorphism in virus metapopulations, which reflect in the topology and statistical properties of local and regional haplotype networks of viral DNA.

CONCLUSIONS

Knowledge on the role played by informal seed systems in the diffusion of crop diseases is essential for implementing efficient control strategies to curb crop disease pandemics. The comparison of anthropological, genetic, and plant epidemiological data provides a unique opportunity to explore how the interplay of social structures and local networks of seed exchange influences regional dynamics of plant viruses.

REFERENCES

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Building bridges between disciplines for sustainable management of plant virus diseases



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